



# Animal Source Identification Using A Cryptosporidium DNA Characterization Technique

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### **NOTICE**

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#### **FOREWORD**

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This publication has been produced as part of the Laboratory's strategic long-term research plan. It is published and made available by EPA's Office of Research and Development to assist the user community and to link researchers with their clients.

Hugh W. McKinnon, Director National Risk Management Research Laboratory

#### **ABSTRACT**

This document summarizes the application of a particular molecular method to improve detection and differentiation of species and genotypes of *Cryptosporidium* oocysts found in environmental samples. Of particular interest is the method's potential for determining the source animal types of oocysts in water samples. The molecular method is a nested polymerase chain reaction (PCR)-restriction fragment length polymorphism (RFLP) procedure that characterizes the small sub-unit (SSU) ribosomal RNA gene. The method was previously developed for characterizing oocyst DNA from clinical samples. The current project explores the method's applicability to environmental water samples, which have greater diversity of oocyst species and strains, lower concentrations of oocysts, and different interferents than clinical samples. Results include demonstrating that the method is capable of detection and differentiation of at least 10 species and 22 genotypes of *Cryptosporidium*; method sensitivity demonstrated to a single oocyst with laboratory samples; and detection and differentiation of oocysts from oyster gill washings and hemolymph, storm water, surface water, and raw waste water. The method's capability to determine an oocyst's source animal type was demonstrated by identification in environmental water samples of host-adapted *Cryptosporidium* species and genotypes that were consistent with the source animal types (i.e., humans, farm animals, wildlife, and/or pets) inhabiting the sampled watersheds.

# TABLE OF CONTENTS

NOTICE	. ii
FOREWORD	. iii
ABSTRACT	. iv
LIST OF FIGURES	. vi
ACKNOWLEDGMENTS	vii
INTRODUCTION	
Cryptosporidiosis and Cryptosporidium  Benefits of Identifying Host Range of Cryptosporidium Oocysts in Water  Determining the Host Range of Oocysts in Water Samples  Developing a Collection of Infection Data for Cryptosporidium-Host Pairs  Methods for Detailed Characterization of Oocysts  Discovery of Correlations Between Characteristics of Oocysts and Their Host Ranges	. 1 . 2 . 2
PROJECT RATIONALE, OBJECTIVES, AND TASKS	. 4
MATERIALS AND METHODS  Materials and Methods for Phylogenetic Analysis of Cryptosporidium Genus Based on SSU rRNA Gene	s
Development Process for SSU rRNA-based Nested PCR-RFLP Method for Cryptosporidium Detection a  Differentiation  Evaluation of SSU rRNA-based Nested PCR-RFLP Method for Cryptosporidium Detection and  Differentiation in Storm Water Samples	and . 5
<b>KEY RESULTS</b> Results of Phylogenetic Analysis of Cryptosporidium Genus Based on SSU rRNA Genes of Five Types of	of
Cryptosporidium  Results of Development of SSU rRNA Nested PCR-RFLP Diagnostic Tool Evaluation of the SSU rRNA-based Nested PCR-RFLP Diagnostic Tool Gill Washings and Hemolymph from Oysters Storm Stream Flow Samples Raw Surface Water Samples Raw Wastewater Samples Comparison of PCR Protocols for Species Detection, Differentiation, and Genotyping of Cryptosporidiu	. 8 10 10 10 11 11
CONCLUSIONS AND RECOMMENDATIONS  Specific Conclusions  General Conclusions  Recommendations  Current problems in molecular detection of Cryptosporidium oocysts  Actions needed to enable routine use of molecular tools in water sample analysis	12 12 14 15
REFERENCES	17
APPENDIX 1 – Molecular Tools	19

## **LIST OF FIGURES**

Figure 1. Detection and Diagnosis of Cryptosporidium Parasites by Nested PCR-RFLP
Figure 2. Phylogenetic Relationships of Cryptosporidium Parasites to Other Apicomplexans(A) and Each Other(B)
(Xiao et al., 1999a) 7
Figure 3. Updated phylogenetic relationship of Cryptosporidium parasites
Figure 4. Detection of Cryptosporidium spp. by SSU rRNA-based Nested PCR
Figure 5. Differentiation of Cryptosporidium Species and Genotypes by SSU rRNA-based PCR-RFLP
Figure 6. Sensitivity of the SSU rRNA-based Cryptosporidium PCR-RFLP Genotyping Technique
Figure 7. Differentiation of the Cryptosporidium Parasites in Storm Water Samples by SSU rRNA-based PCR-
RFLP11

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